

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1-25. (canceled)

26. (currently amended) A method for analyzing or amplifying a nucleic acid sequence, comprising analyzing or amplifying a nucleic acid with an S3P primer, comprising at least part of a consensus sequence of a splice-site border sequence, and at least one AFLP primer which contains at least one selective nucleotide at its 3' end,

wherein the nucleic acid sequence comprises a restriction fragment with one oligonucleotide adapter at both ends, and

wherein said restriction fragment is derived from genomic DNA, mitochondrial DNA, chloroplast DNA, or recombinant DNA.

27-28. (canceled)

29. (currently amended) The method according to claim [[28]] 26, in which the restriction fragment to which the adapter sequence has been ligated is part of a mixture of adapter-ligated restriction fragments.

30. (previously presented) The method according to claim 26, in which the nucleic acid sequence contains or is

suspected to contain, an intron-exon junction and/or a splice site.

31. (canceled)

32. (previously presented) The method according to claim 26, wherein the S3P primer is in an intron-to-exon orientation or in an exon-to-intron orientation.

33-34. (canceled)

35. (currently amended) The method according to claim [[34]] 26, wherein the S3P primer further comprises a random sequence.

36. (previously presented) The method according to claim 26, wherein S3P primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

37. (previously presented) The method according to claim 26, wherein the S3P primer contains a total of between 8 and 20 nucleotides.

38. (previously presented) The method according to claim 26, wherein between 4 and 10 nucleotides present in the S3P primer are complementary to the conserved region or consensus sequence of the splice site.

39. (currently amended) The method according to claim 26, wherein the consensus sequence is $X_1X_2GTX_3X_4X_5X_6$, wherein X_1 ,

X_2 , X_3 , X_4 , X_5 , X_6 are independently selected from the group consisting of A,C,T, [[or]] and G.

40. (previously presented) The method according to claim 39, wherein the consensus sequence is AGGTAAGT.

41. (currently amended) A method for analyzing a nucleic acid sequence, comprising:

(a) amplifying an adapter-ligated restriction fragment generated from the nucleic acid to be analysed, using one or more S3P-primers, comprising at least part of a consensus sequence of a splice-site border sequence, and optionally an at least one AFLP-primer which contains at least one selective nucleotide at its 3' end to amplify the nucleic acid sequence; and optionally comprising the further step of:

(b) detecting the amplified nucleic acid sequences thus obtained.

42. (currently amended) A method for analyzing a nucleic acid sequence, the method comprising the steps of:

(a) ~~restricting the~~ treating a starting nucleic acid with a restriction endonuclease to provide a mixture of restriction fragments;

(b) ligating the restriction fragments thus obtained to at least one adapter;

(c) amplifying the mixture of adapter-ligated restriction fragments thus obtained with one or more S3P-primers, comprising at least part of a consensus sequence of a splice-site

border sequence, and optionally at least one AFLP-primer which contains at least one selective nucleotide at its 3' end to provide a mixture of amplified restriction fragments; and
optionally comprising the further step of

(d) detecting the amplified restriction fragments thus obtained.

43. (currently amended) A method for the amplification of at least one restriction fragment obtained from a starting DNA, comprising:

(a) digesting the starting DNA with at least one restriction endonuclease, thereby providing one or more restriction fragments;

(b) ligating at least one oligonucleotide adapter to ~~one~~ or both ends of the restriction fragments to provide adapter-ligated restriction fragments;

(c) providing a primer set comprising one or more S3P primers, comprising at least part of a consensus sequence of a splice-site border sequence, and optionally at least one AFLP primer;

(d) contacting the adapter-ligated restriction fragments with the set of primers;

(e) amplifying the adapter-ligated restriction fragments with the set of primers; and

(f) recovery of any amplified DNA fragments.

44-47. (canceled)

48. (currently amended) [[A]] The method for the enrichment of a sample for nuclear or organelle derived amplification products, comprising enriching the sample according to a method according to claim 43, wherein at least two different S3P primer sets are utilized.

49. (previously presented) The method according to claim 41, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

50. (previously presented) The method according to claim 42, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

51. (previously presented) The method according to claim 43, wherein the S3P-primer is specific for a splice site selected from the group consisting of GU-AG introns, AU-AC introns, Group I introns, Group II introns, Group III introns, Twintrons, Pre-tRNA introns, and splice sites that are identified using computer based splice site identification methods.

52-54. (canceled)